



**FUNDAMENTAL RESEARCH AT THE [BIO:INFO:MICRO]
INTERFACE**



**High-resolution analysis and modeling of temporal and
spatial patterns of biological control circuits**

**Stanford University
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High-resolution analysis and modeling of temporal and spatial patterns of biological control circuits

Interdisciplinary Stanford University team

Harley McAdams (PI)	Developmental Biology
Stanley Cohen	Genetics
Stephen Smith	Mol. & Cell. Physiology
Lucy Shapiro	Developmental Biology
Matthew Scott	Developmental Biology
James Harris	Electrical Engineering
Olav Solgaard	Electrical Engineering
Martin Morf	Electrical Engineering
Claire Tomlin	Aeronautics/Astronautics
W. E. Moerner	Chemistry



High-resolution analysis and modeling of temporal and spatial patterns of biological control circuits

Overall objective

Analyze fundamental mechanisms regulating the cell cycle and cellular differentiation, including differentiation of multicellular organisms with a program of

- **Enabling instrumentation technologies**
- **Informatics and biosimulation advances**
- **Biological studies**



Factors Driving Biological Progress

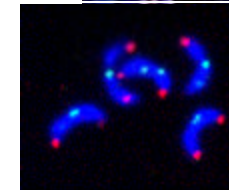
- Robotics, nanotechnology, and optoelectronics applied to high-throughput experimental instrumentation



- Bioinformatics



- Fluorescent tagging of bio-molecules and *in vivo* imagery



- Coupling of bacterial studies with studies of parallel questions in embryos to exploit evolutionary conservation of mechanisms

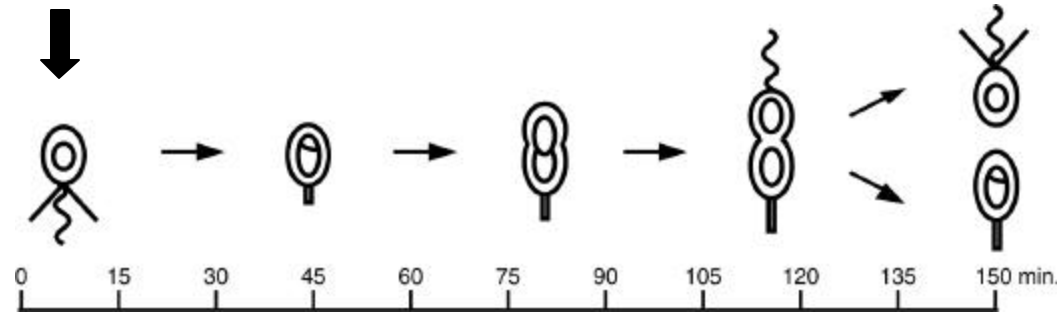


Collaborations

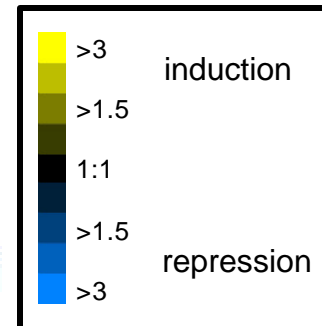
McAdams/Shapiro	<ul style="list-style-type: none">• Apply gene expression microarrays to deduce the complete regulatory circuit controlling cell cycle and asymmetric division in a bacterium, <i>Caulobacter crescentus</i>, with 3,400 genes
Moerner/Shapiro	<ul style="list-style-type: none">• Apply high-resolution in vivo fluorescent microscopy to characterize mechanisms that localize regulatory proteins in <i>Caulobacter crescentus</i>
Smith/Harris	<ul style="list-style-type: none">• Develop low-cost, fluorescence reader/microscope integrated on a single-chip for field-deployable bioassay instruments
Smith Scott/Cohen/	<ul style="list-style-type: none">• 10X enhancement of 2-photon microscopy throughput and application to time-lapse imaging of development in living embryos and bacterial colonies
Scott/Solgaard	<ul style="list-style-type: none">• Develop nanotechnology-based instrument to inject aliquots of regulatory molecules into specifically-targeted cells of 1000 <i>Drosophila</i> embryos per hour
Cohen/McAdams	<ul style="list-style-type: none">• Apply artificial intelligence and genetic simulation technologies to deduce genetic circuitry from gene expression microarray data
Tomlin/McAdams/Morf	<ul style="list-style-type: none">• Apply hybrid control theory and logic synthesis to analysis of control systems guiding somatic development in <i>Drosophila</i> embryos and other multicellular systems

Cell Cycle Time Course

synchronize cells



- collect **RNA** every 15 min. for 150 min.
- hybridize each time point to common **reference RNA** derived from a mixed, unsynchronized culture



2966 expression profiles



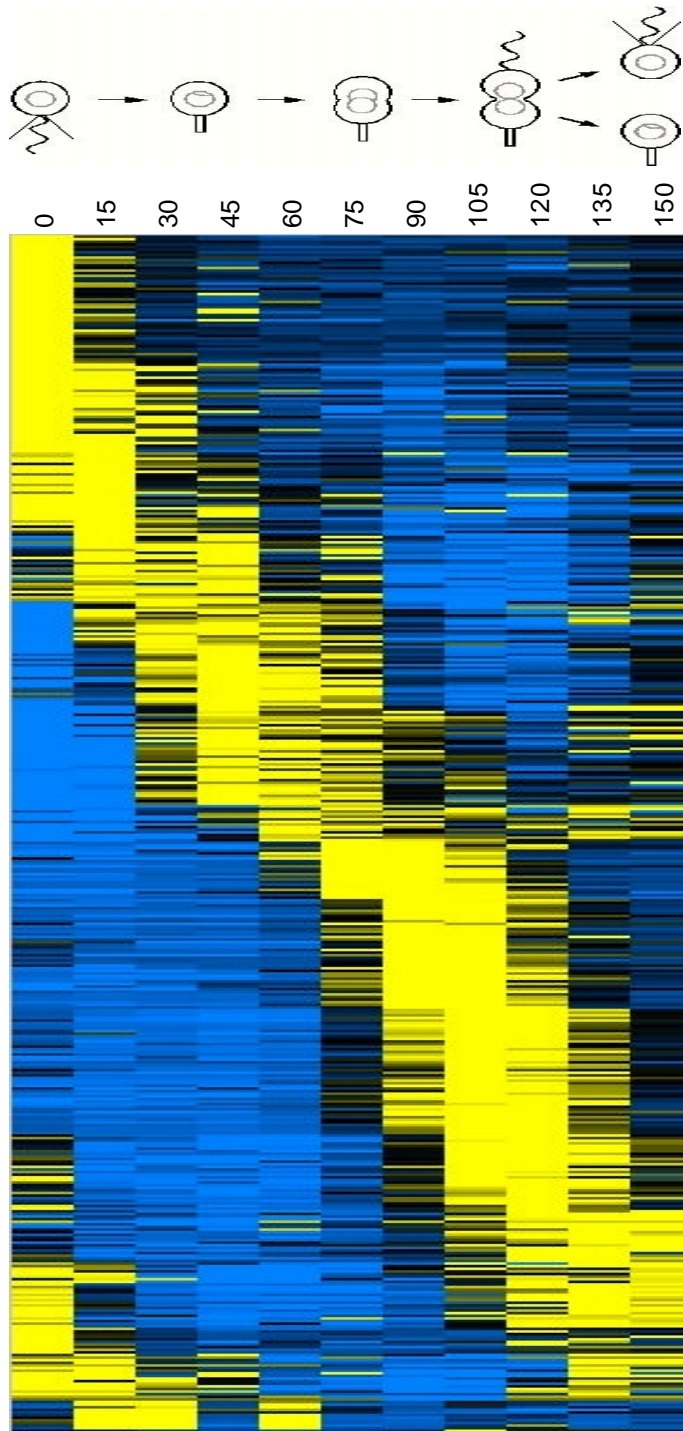
553 cell cycle-dependent transcripts → clustering analysis

Microarrays

- Michael Laub

Caulobacter genome sequence

- The Institute for Genome Research (TIGR)



heat shock/
stress

G1

late G1

S

late S / early G2

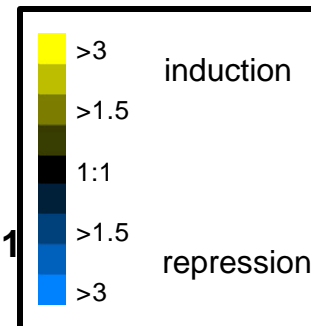
G2


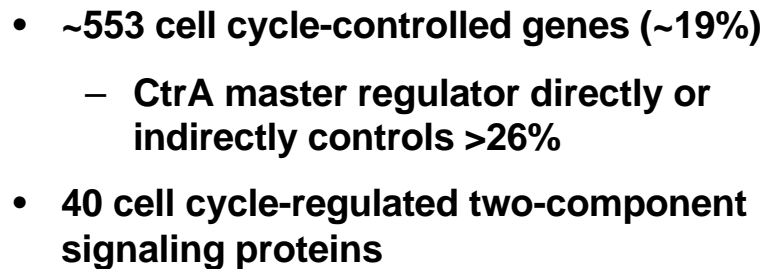
late G2 / early G1

Experimental Tactics

- Expression profiles of mutants versus wild type
- Expression profiles of wild type under different conditions
- Identify common promoter motifs in temporally co-regulated genes

Relative RNA levels

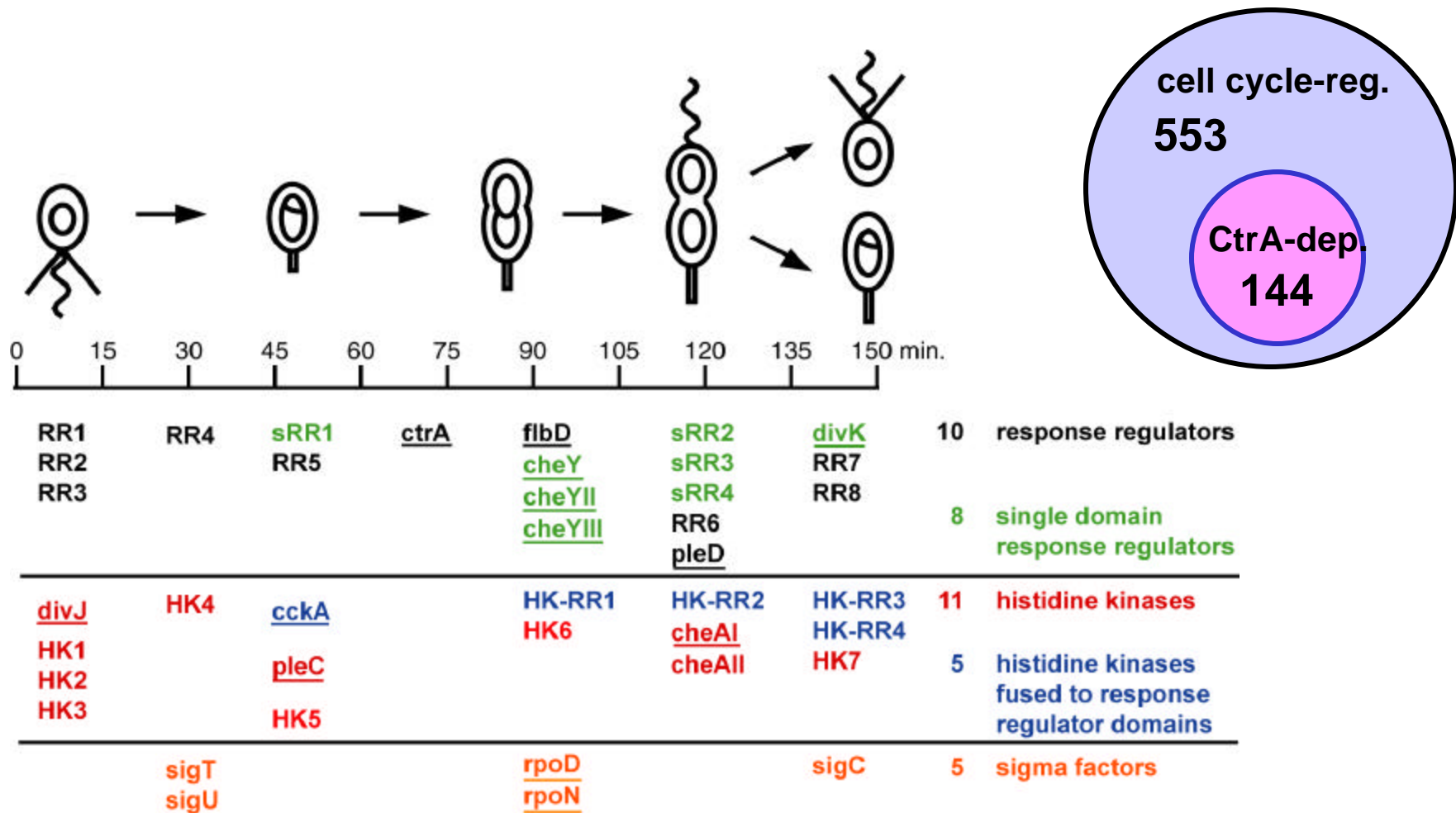




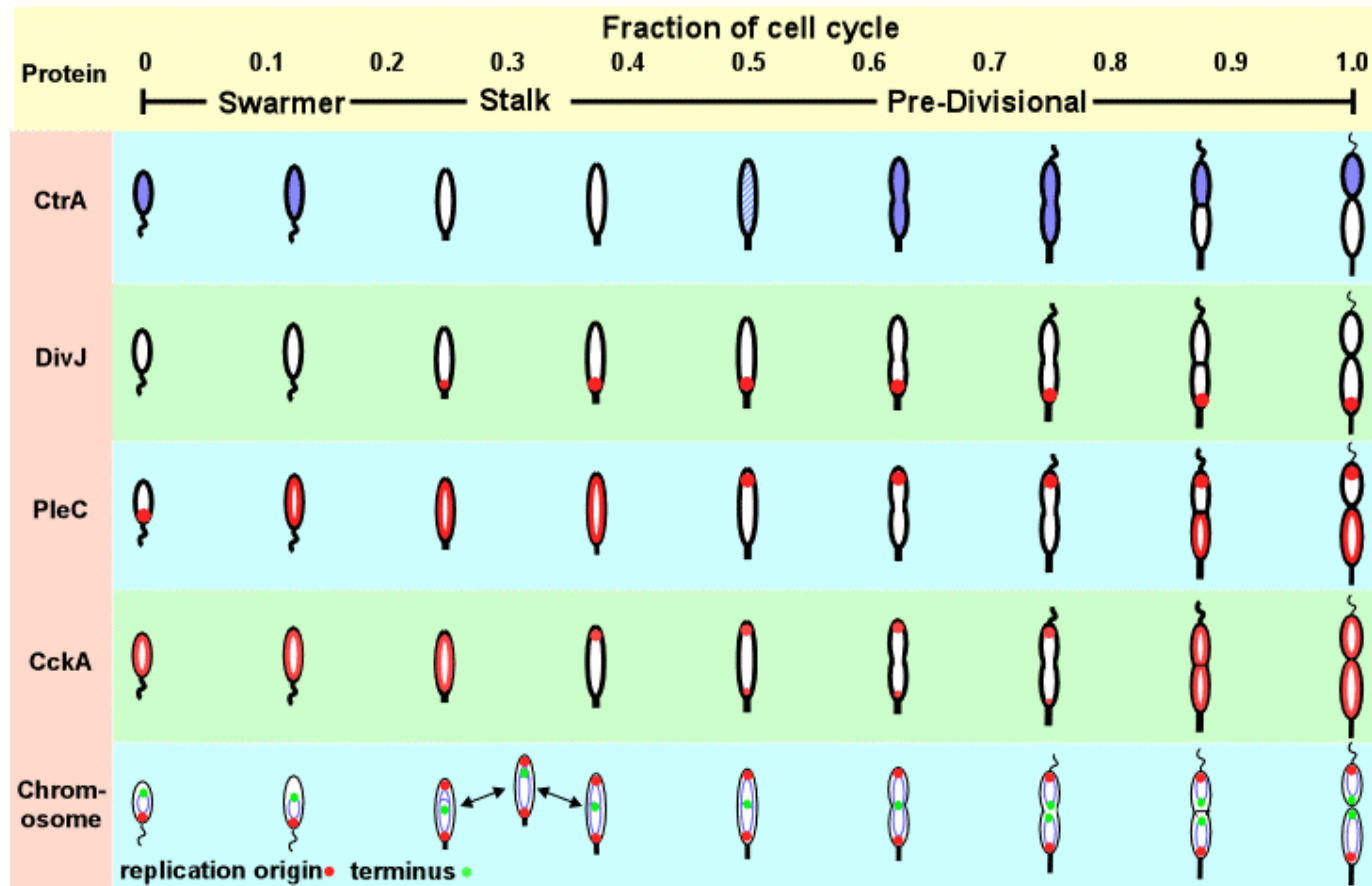
Objective of this project: identify the complete regulatory circuitry controlling a bacterial cell cycle



Cell Cycle-Regulated Regulatory Genes



Key regulatory proteins are both spatially and temporally regulated . . .



Key questions

- Mechanism for localization
- Structures at the membrane
- Reactions and reaction kinetics